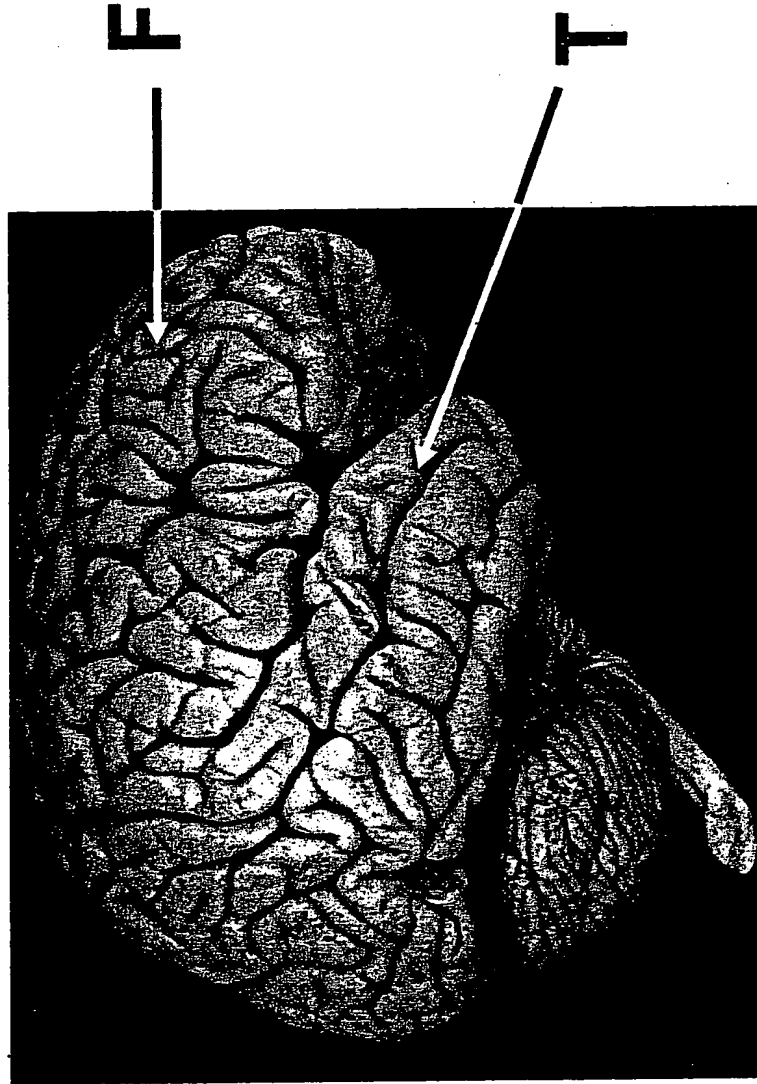


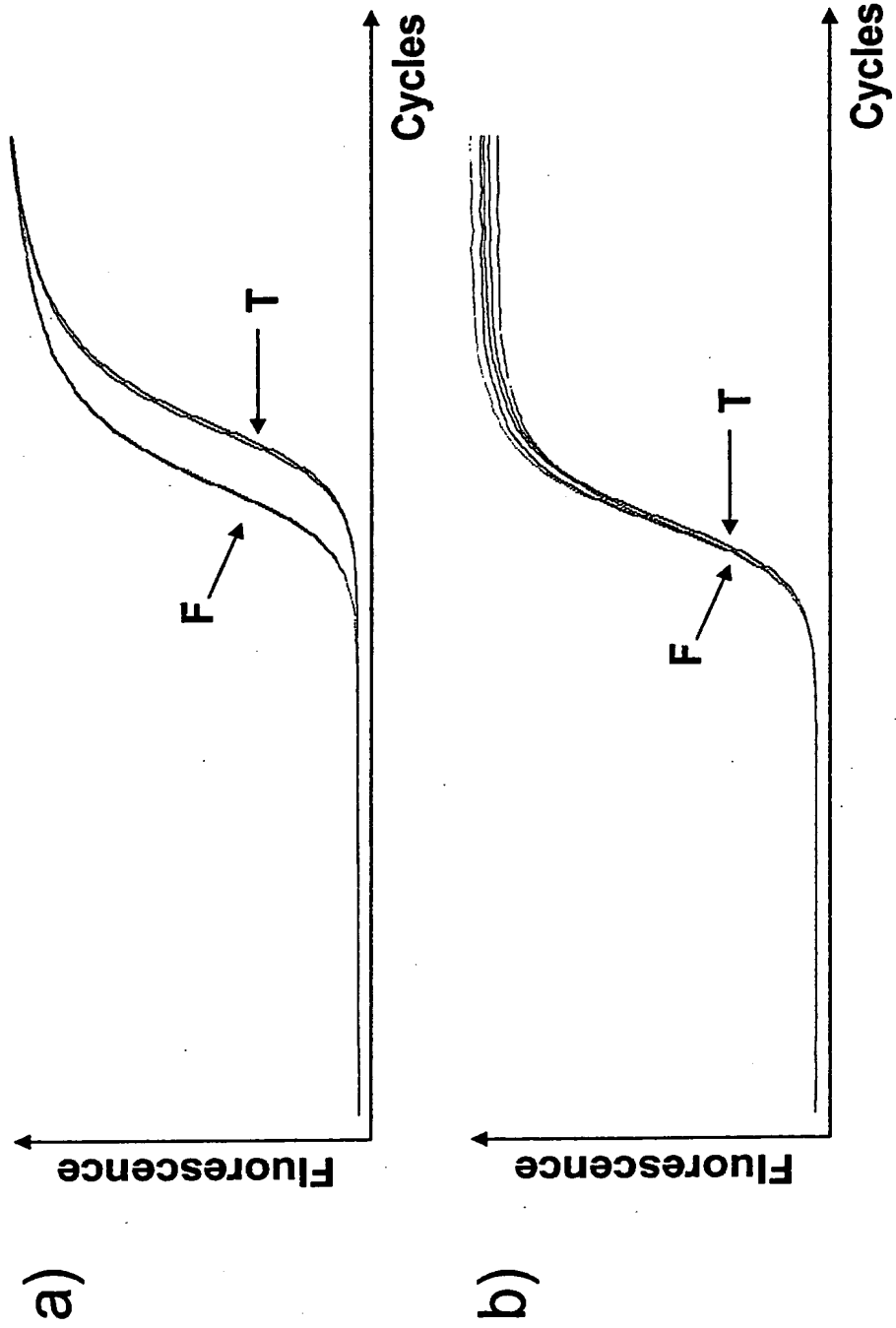
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**Fig. 1: Identification of Genes Involved  
in Alzheimer's Disease Pathology**



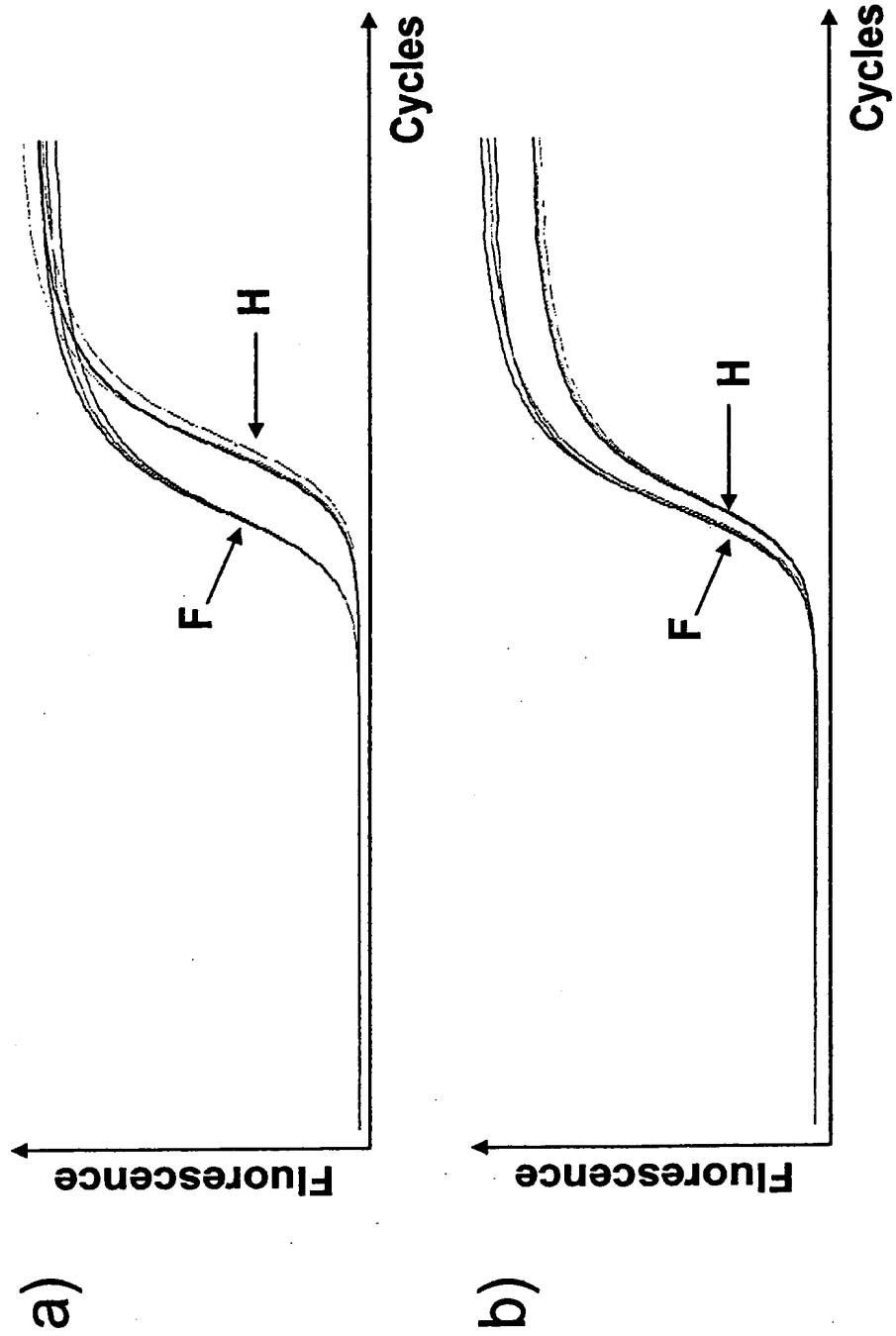
-2/14-

**Fig. 2: Verification of differential expression of human TARPP by quantitative RT-PCR**



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**Fig. 3: Verification of differential expression of human TARPP by quantitative RT-PCR**



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**Fig. 4 : SEQ ID NO. 1: amino acid sequence of human TARPP protein****Length: 813 aa**

1 MSEQGDNLQA IAEEGGTEQE TATPENGIVK SESLDEEEKL ELQRRLEAQN  
51 QERRKSKSGA GKGKLTRSLA VCEESSARPG GESLQDQESI HLQLSSFSSSL  
101 QEEDKSRKDD SEREKEKDKN KDKTSEKPKI RMLSKDCSQE YTDSTGIDLH  
151 EFLINTLKNN SRDRMILLKM EQEIIDFIAD NNNHYKKFPQ MSSYQRMLVH  
201 RVAAYFGLDH NVDQTGKSVI INKTSSTRIP EQRFCHEHLKD EKGEESQKRF  
251 ILKRDNSSID KEDNQSVCSQ ESLFVENSRL LEDSNICNET YKKRQLFRGN  
301 RDGSGRTSGS RQSSSENELK WSDHQRAWSS TSDSDSSNRNL KPAMTKTASF  
351 GGITVLTRGD STSSTRSTGK LSKAGSESSS SAGSSGSLSR THPPLQSTPL  
401 VSGVAAGSPG CVPYPENGIG GQVAPSSTSY ILLPLEAATG IPPGSILLNP  
451 HTGQPFVNPDP GTPAIYNPPT SQQPLRSAMV GQSQQQPPQQ QPSPQPQQQV  
501 QPPQPQMAGP LVTQSVQGLQ ASSQSVQYPA VSFPQHLHP VSPTQHFPMR  
551 DDVATQFGQM TLRQSSGET PEPPSGPVYP SSLMPQPAQQ PSYVIASTGQ  
601 QLPTGGFSGS GPPISQQVLQ PPPSPQGFVQ QPPPAQMPVY YYPSGQYPTS  
651 TTQQYRPMAP VQYNAQRSQQ MPQAAQQAGY QPVLSGQQGF QGLIGVQQPP  
701 QSQNVINNQQ GTPVQSVQSV YPTMSSYQVP MTQGSQGLPQ QSYQQPIMLP  
751 NQAGQGSLPA TGMPVYCNVT PPTPQNNLRL IGPHCPSTV PVMSASCRTN  
801 CASMSNAGWQ VKF\*

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**Fig. 5: Alignment of SEQ ID NO. 1human  
TARPP, with mouse TARPP**

Length: 813 aa

```

1  MSEQGDNLNQAIAEEGGTEQETATPENGIVKSESLDEEEKLELQRRLEAQN 50
   ||||| | | ||| | | . | ||||| . ||||| ||||| ||||| |||||
1  MSEQGGLTPTILEEGQTEPESA . PENGILKSESLDEEEKLELQRRLAAQN 49

51  QERRKSKSGAGKGKLTRSLAVCEESSARPGGESLQDQESIHLQLSSFSSL 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50  QERRKSKSGAGKGKLTRSLAVCEESSARSGGESHQDQESIHLQLSSFPSL 99

101  QEEDKSRKDDSEREKEKDKNKDKTSEKPKIRMLSKDCSQEYTDSTGIDLH 150
     ||||| ||||| ||||| ||||| :: ||: ||||| ||||| ||||| |||||
100  QEEDKSRKDDSEREKEKDKNREKLSEKPKIRMLSKDCSQEYTDSTGIDLH 149

151  EFLINTLKNNSRDRMILLKMEQEIIDFIADNNNHKKFPQMSSYQRMVLVH 200
     ||||| ||||| ||||| ||||| . ||||| . ||||| ||||| |||||
150  GFLINTLKNNSRDRMILLKMEQEMIDFIADSNNHKKFPQMSSYQRMVLVH 199

201  RVAAYFGLDHNVDQTGKSVIINKTSSTRIPEQRFCEHLKDEKGEESQKRF 250
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200  RVAAYFGLDHNVDQTGKSVIINKTSSTRIPEQRFCEHLKDEKSEESQKRF 249

251  ILKRDNSSIDKEDNQ.....SV 267
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250  ILKRDNSSIDKEDNQNRMHPPFRDDRRSKSIEEEEEYQVRERIFAHDSV 299

268  CSQESLFFVENSRLLEDNICNETYKKRQLFRGNRDGSGRTSGSRQSSSEN 317
     ||||| .: |||| || . ||||| ||||| ||||| . || ||||| |||||
300  CSQESLFLDNSRLQEDMHICNETYKKRQLFRAHRDSSGRTSGSRQSSSET 349

318  ELKWSDHQRAWSSSTDSDSSNRNLKPAMTKTASFGGITVLTRGDSTSSTRS 367
     ||: | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350  ELRWPDHQRAWSSSTDSDSSNRNLKPMTTKTASFGGITVLTRGDSTSSTRS 399

368  TGKLSKAGSESSSSAGSSGSLSRTHPPLQSTPLVSGVAAGSPGCVYPYEN 417
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| . | |||
400  AGKLSKTGSESSSSAGSSGSLSRTHP..QSTALTSSVAAGSPGCMAYSEN 447

418  GIGGQVAPSSTSYILLPLEAATGIPPGSILLNPHTGQPFVNPDPGTPAIYN 467
     |. ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448  GMGGQVPPSSTSYILLPLESATGIPPGSILLNPHTGQPFVNPDPGTPAIYN 497

468  PPTSQQPLRSAMVGQSQQQPPQQQSPQPPQQQVQPPQPMAGPLVTQSVQ 517
     || |||| || | . || ||||| ||||| ||||| ||||| ||||| |||||
498  PPGSQQTLRGTVGGQ . PQQPPQQQSPQPPQQQVQASQPMAGPLVTQ... 543

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518 GLQASSQSVQYPAVSFPPQHLLPVSPQHFPMRDDVATQFGQMTLSRQSS 567
      |:::| || |:::| || ||
544 .....REELAAQFSQLSMSRQSS 561

568 GETPEPPSGPVYPSSLMPQPAQQPSYVIASTGQQLPTGGFSGSGPPISQQ 617
      |:||||| |||.||:| || |||| | |||| | |||||
562 GDTPEPPSGTVYPASLLPQTAQPQSYVITSAGQQLSTGGFSDSGPPISQQ 611

618 VLQPPPSPOGFVQQPPPAQMPVYYYPSGQYPTSTTQQYRPMAPVQYNAQR 667
      ||| ||||| ||||| ||||| ||||| |||||.|||:| |||.||
612 VLQAPPSPOGFVQQPPPAQMSVYYYPSGQYPTSTSQQYRPLASVQYSAQR 661

668 SQQMPQAAQQAGYQPVLSGQQGFQGLIGVQQPPQSONVINNQOGTPVQSV 717
      |||.|| ||||| ||||| |||||:|.||| || |...||| || |
662 SQQIPQTTQQAGYQPVLSGQQGFQGMMGVQQSAHSQGVMSQQGAPVHGV 711

718 MVSYPMTSSYQVPMTQGSQGLPQQSYQQPIMLPNQAGQGSLPATGMPVYC 767
      ||||| ||||| ||||| |||||.||| |||||.||| ||||| |||||
712 MVSYPMTSSYQVPMTQGSQAVPQQTYQPPIMLPNQAGQGSLPATGMPVYC 761

768 NVTPTPQNNLRLIGPHCPSSSTVPVMSASCRTNCASMSNAGWQVKF 813
      ||||| ||||| ||||| ||||| ||||| |||||.||| |||||
762 NVTPPNPQNNLRLMGPHCPSSSTVPVMSASCRTNCGNVSNAGWQVKF 807

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**Fig. 6: SEQ ID NO. 2: nucleotide sequence of human TARPP coding sequence**

Length: 2442 bp

```

1  ATGTCTGAGC AAGGAGACCT GAATCAGGCA ATAGCAGAGG AAGGAGGGAC
51  TGAGCAGGAG ACGGCCACTC CAGAGAACGG CATTGTAAAA TCAGAAAGTC
101 TGGATGAAGA GGAGAAACTG GAACTGCAGA GGCGGCTGGA GGCTCAGAAT
151 CAAGAAAGAA GAAAATCCAA GTCAGGAGCA GGAAAAGGTA AACTGACTCG
201 CAGYCTTGCT GTCTGTGAGG AATCTTCTGC CAGACCAGGA GGTGAAAGTC
251 TTCAGGATCA GGAATCAATT CATTACAGC TTTCCAGTTT TTCCAGCCTG
301 CAAGAGGAGG ATAAATCTAG GAAAGATGAC TCTGAAAGAG AAAAAGAAAA
351 GGATAAAAAA AAAGATAAAA CCTCTGAAAA ACCCAAGATC AGAATGTTAT
401 CAAAAGATTG CAGCCAAGAA TACACGGATT CTACAGGCAT AGACTTACAC
451 GAGTTTCTGA TTAACACATT AAAGAATAAT TCCAGGGACA GGATGATACT
501 TTTGAAATG GAGCAGGAAA TTATTGATTT CATTGCTGAC AACATAATC
551 ATTATAAAAA GTTCCCTCAG ATGTCATCGT ATCAGAGGAT GCTTGTCCAT
601 CGAGTGGCAG CTTATTTTGG ATTGGATCAC AATGTGGATC AAACAGGAAA
651 ATCTGTTATC ATCAACAAGA CCAGCAGCAC CAGAATACCA GAGCAAAGGT
701 TTTGTGAACA TTTAAAAGAT GAAAAAGGTG AAGAATCCCA GAAGCGGTTT
751 ATCTTGAAGC GAGATAACTC TAGTATTGAT AAAGAAGACA ATCAGTCAGT
801 TTGCTCCCAG GAAAGCCTTT TTGTGGAAAA CAGTAGGCTC TTGGAAGACA
851 GTAACATATG CAATGAGACC TATAAGAAAA GACAGCTCTT TCGGGGCAAC
901 AGAGATGGCT CAGGGAGAAC ATCTGGGAGT CGACAGAGCA GCTCAGAAAA
951 TGAACTCAAG TGGTCTGACC ACCAAAGGGC CTGGAGCAGC ACAGACTCCG
1001 ACAGTTCCAA CCGCAATCTA AAGCCCGCCA TGACCAAGAC GGCGAGTTTT
1051 GGGGGCATCA CGGTGCTGAC CAGGGGTGAC AGCACTTCCA GTACTAGGAG
1101 TACCGGAAG CTGTCCAAAG CAGGTTCCGA GTCTTCCAGC AGTGCAGGCT
1151 CCTCAGGATC GCTGTCCCGC ACCCATCCAC CTCTCCAGAG CACACCCCTA
1201 GTCTCAGGTG TGGCAGCTGG CTCTCCAGGC TGTGTGCCTT ATCCAGAGAA
1251 TGGAATAGGG GGCCAGGTTG CTCCCAGCAG CACCAGCTAC ATCCTCCTTC
1301 CACTTGAAGC TGCAACAGGC ATCCCGCCTG GAAGCATCCT TCTTAATCCA
1351 CACACAGGCC AGCCCTTTGT GAATCCCGAT GGAACCTCTG CAATATACAA
1401 CCCACCCACC AGTCAGCAGC CCCTGCGAAG CGCCATGGTG GGGCAGTCCC
1451 AACAGCAGCC GCCACAGCAG CAGCCCTCCC CGCAGCCCCA ACAGCAGGTC
1501 CAGCCACCGC AGCCACAGAT GGCAGGCCCT CTGGTCACTC AGTCTGTCCA
1551 GGGGCTGCAG GCTTCCTCCC AGTCAGTGCA ATATCCGGCA GTCTCTTTTC
1601 CTCCCCAGCA CCTCCTACCT GTGTCTCCAA CGCAGCACTT TCCCATGAGA
1651 GATGATGTGG CAACACAGTT TGGCCAGATG ACCCTGAGCC GGCAGTCCTC
1701 GGGGGAGACT CCTGAACCCC CATCAGGTCC TGTCTACCCA TCCTCCCTTA
1751 TGCCACAGCC GGCCCAGCAG CCCAGCTATG TAATCGCCTC TACAGGCCAG
1801 CAGCTTCCTA CAGGAGGATT CTCAGGCTCT GGCCCTCCCA TCTCCAGCA
1851 GGTCTCTCAG CCCCCTCCCT CACCACAGGG ATTCTGTCAA CAGCCTCCGC
1901 CTGCACAGAT GCCTGTATAT TATTACCCAT CTGGTCAGTA CCCTACCTCA
1951 ACCACGCAAC AGTACCGGCC CATGGCCCCG GTTCAGTACA ACGCTCAGAG
2001 GAGTCAACAG ATGCCACAGG CAGCACAGCA AGCAGGTTAC CAGCCAGTCT
2051 TGTCTGGTCA ACAGGGATTG CAAGGCCTAA TAGGAGTGCA GCAGCCACCT
2101 CAGAGTCAGA ACGTGATAAA TAACCAACAA GGAACCTCCG TGCAAAGCGT
2151 GATGGTTTCC TACCCAACAA TGTCTTCTTA TCAGGTGCCA ATGACCCAGG
2201 GTTCTCAAGG ACTGCCCCAG CAGTCATACC AACAGCCAAT CATGTTACCT
2251 AATCCAGCAG GTCAAGGGTC ACTCCAGGCC ACTGGAATGC CTGTTTACTG
2301 TAATGTCACA CCGCCCACCC CTCAGAACAA CCTTAGGCTG ATTGGCCCAC
2351 ACTGCCCCTC CAGCACTGTC CCAGTGATGT CAGCTAGCTG CAGAACAAC
2401 TGTGCAAGTA TGAGCAATGC TGGTTGGCAG GTCAAATTCT GA

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**Fig. 7: SEQ ID NO. 3: nucleotide sequence of human TARPP cDNA**

**Length: 3212 bp**

```

1  GTGATTTGCT  GGAAGCTGGT  CATTAGTGTT  GACGATGTGT  CACACTGTGT
51  AAGGGAATCG  CATGGAGATG  GGCATTCCGA  ACTGTTAATG  GGGACATGGG
101  ACTCCAGTTG  TCTCTGATCA  CTTGTGTGGA  TTTTCCTGGC  GTAGAACGAC
151  AGAAGCCGCT  AGTAAGTCGC  CAAGACCTAC  AGCAGGAATT  CTGCACCAAA
201  GGGCATAAAA  TCTTGTTATT  TTAATTGCA  TCTGGGAGAA  TGTCTGAGCA
251  AGGAGACCTG  AATCAGGCAA  TAGCAGAGGA  AGGAGGGACT  GAGCAGGAGA
301  CGGCCACTCC  AGAGAACGGC  ATTGTTAAAT  CAGAAAGTCT  GGATGAAGAG
351  GAGAAACTGG  AACTGCAGAG  GCGGCTGGAG  GCTCAGAATC  AAGAAAGAAG
401  AAAATCCAAG  TCAGGAGCAG  GAAAAGGTAA  ACTGACTCGC  AGYCTTGCTG
451  TCTGTGAGGA  ATCTTCTGCC  AGACCAGGAG  GTGAAAGTCT  TCAGGATCAG
501  GAATCAATTC  ATTTACAGCT  TTCCAGTTTT  TCCAGCCTGC  AAGAGGAGGA
551  TAAATCTAGG  AAAGATGACT  CTGAAAGAGA  AAAAGAAAAG  GATAAAAACA
601  AAGATAAAAC  CTCTGAAAAA  CCCAAGATCA  GAATGTTATC  AAAAGATTGC
651  AGCCAAGAAT  ACACGGATTC  TACAGGCATA  GACTTACACG  AGTTTCTGAT
701  TAACACATTA  AAGAATAATT  CCAGGGACAG  GATGATACTT  TTGAAAATGG
751  AGCAGGAAAT  TATTGATTTC  ATTGCTGACA  ACAATAATCA  TTATAAAAAG
801  TTCCCTCAGA  TGTCATCGTA  TCAGAGGATG  CTTGTCCATC  GAGTGGCAGC
851  TTATTTTGGG  TTGGATCACA  ATGTGGATCA  AACAGGAAAA  TCTGTTATCA
901  TCAACAAGAC  CAGCAGCACC  AGAATACCAG  AGCAAAGGTT  TTGTGAACAT
951  TTAAAAGATG  AAAAAGGTGA  AGAATCCCAG  AAGCGGTTTA  TCTTGAAGCG
1001  AGATAACTCT  AGTATTGATA  AAGAAGACAA  TCAGTCAGTT  TGCTCCCAGG
1051  AAAGCCTTTT  TGTGGAAAAC  AGTAGGCTCT  TGGAAGACAG  TAACATATGC
1101  AATGAGACCT  ATAAGAAAAG  ACAGCTCTTT  CGGGGCAACA  GAGATGGCTC
1151  AGGGAGAACA  TCTGGGAGTC  GACAGAGCAG  CTCAGAAAAT  GAACTCAAGT
1201  GGTCTGACCA  CCAAAGGGCC  TGGAGCAGCA  CAGACTCCGA  CAGTTCCAAC
1251  CGCAATCTAA  AGCCCGCCAT  GACCAAGACG  GCGAGTTTTG  GGGGCATCAC
1301  GGTGCTGACC  AGGGGTGACA  GCACTTCCAG  TACTAGGAGT  ACCGGGAAGC
1351  TGTCCAAAGC  AGGTTCCGAG  TCTTCCAGCA  GTGCAGGCTC  CTCAGGATCG
1401  CTGTCCCACA  CCCATCCACC  TCTCCAGAGC  ACACCCCTAG  TCTCAGGTGT
1451  GGCAGCTGGC  TCTCCAGGCT  GTGTGCCTTA  TCCAGAGAAT  GGAATAGGGG
1501  GCCAGGTTGC  TCCCAGCAGC  ACCAGCTACA  TCCTCCTTCC  ACTTGAAGCT
1551  GCAACAGGCA  TCCCGCCTGG  AAGCATCCTT  CTTAATCCAC  ACACAGGCCA
1601  GCCCTTTGTG  AATCCCGATG  GAACTCCTGC  AATATACAAC  CCACCCACCA
1651  GTCAGCAGCC  CCTGCGAAGC  GCCATGGTGG  GGCAGTCCCA  ACAGCAGCCG
1701  CCACAGCAGC  AGCCCTCCCC  GCAGCCCCAA  CAGCAGGTCC  AGCCACCGCA
1751  GCCACAGATG  GCAGGCCCTC  TGGTCACTCA  GTCTGTCCAG  GGGCTGCAGG
1801  CTCCTCCCA  GTCAGTGCAA  TATCCGGCAG  TCTCTTTTCC  TCCCAGCAC
1851  CTCCTACCTG  TGTCTCCAAC  GCAGCACTTT  CCCATGAGAG  ATGATGTGGC
1901  AACACAGTTT  GGCCAGATGA  CCCTGAGCCG  GCAGTCCTCG  GGGGAGACTC
1951  CTGAACCCCC  ATCAGGTCCT  GTCTACCCAT  CCTCCCTTAT  GCCACAGCCG
2001  GCCCAGCAGC  CCAGCTATGT  AATCGCCTCT  ACAGGCCAGC  AGCTTCCTAC
2051  AGGAGGATTG  TCAGGCTCTG  GGCCTCCCAT  CTCCCAGCAG  GTCCTCCAGC
2101  CCCCTCCCTC  ACCACAGGGA  TTCGTGCAAC  AGCCTCCGCC  TGCACAGATG
2151  CCTGTATATT  ATTACCCATC  TGGTCAGTAC  CCTACCTCAA  CCACGCAACA
2201  GTACCGGCCC  ATGGCCCCGG  TTCAGTACAA  CGCTCAGAGG  AGTCAACAGA
2251  TGCCACAGGC  AGCACAGCAA  GCAGGTTACC  AGCCAGTCTT  GTCTGGTCAA
2301  CAGGGATTCC  AAGGCCTAAT  AGGAGTGCAG  CAGCCACCTC  AGAGTCAGAA

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2351 CGTGATAAAT AACCAACAAG GAACTCCGGT GCAAAGCGTG ATGGTTTCCT
2401 ACCCAACAAT GTCTTCTTAT CAGGTGCCAA TGACCCAGGG TTCTCAAGGA
2451 CTGCCCCAGC AGTCATACCA ACAGCCAATC ATGCTACCTA ACCAGGCAGG
2501 TCAAGGGTCA CTCCCAGCCA CTGGAATGCC TGTTTACTGT AATGTCACAC
2551 CGCCCACCCC TCAGAACAAC CTTAGGCTGA TTGGCCCACA CTGCCCCCTCC
2601 AGCACTGTCC CAGTGATGTC AGCTAGCTGC AGAACAACT GTGCAAGTAT
2651 GAGCAATGCT GGTGCGCAGG TCAAATTCTG AGAGCTCTGG CTGTGGTACA
2701 TTTCTTCAGA TATTTCTCAT GGCCTTTGAT GGAAGAGGAA CAAGGTGGGA
2751 AAACCTGGCTG AGGACTTAAG TATTCACTCA ACACTCAAAT GATTGCTGCT
2801 GGTATTCTGT AAAAAGTAAA CAAAGACTAA TATACACGTT AGCTGGTTAA
2851 TGGTGATAT TTCTGTCATG TCTGCTAGGT ATGCCTTTAT AGCTTAGCTA
2901 GTGACATGAA TTCATCAAGG TAAGATTCTC TCCTACCACT GAATACCACT
2951 GTGTAGATTA TAATATCCCT AATTTGGATT AGTTTTGTAC TTTGTGTTGA
3001 GTTTGTGATG CTAAAAGTAT TTAAAAATTA TATACTAAAT CACATTGTAC
3051 CAAAGCTGTA ATGGAAAAGC AAAGAAGAAC TGATGAATTG AAGGAATAAT
3101 TTATATACAT TATAGAGTTT TCTTTTTTAA TGGATATATA CTGTATTGTA
3151 GTGTTTAAATC AAAATAAAAC TATTTGACCT TATGGAGGAA GGTGATGTTT
3201 TTACCACTAA AA
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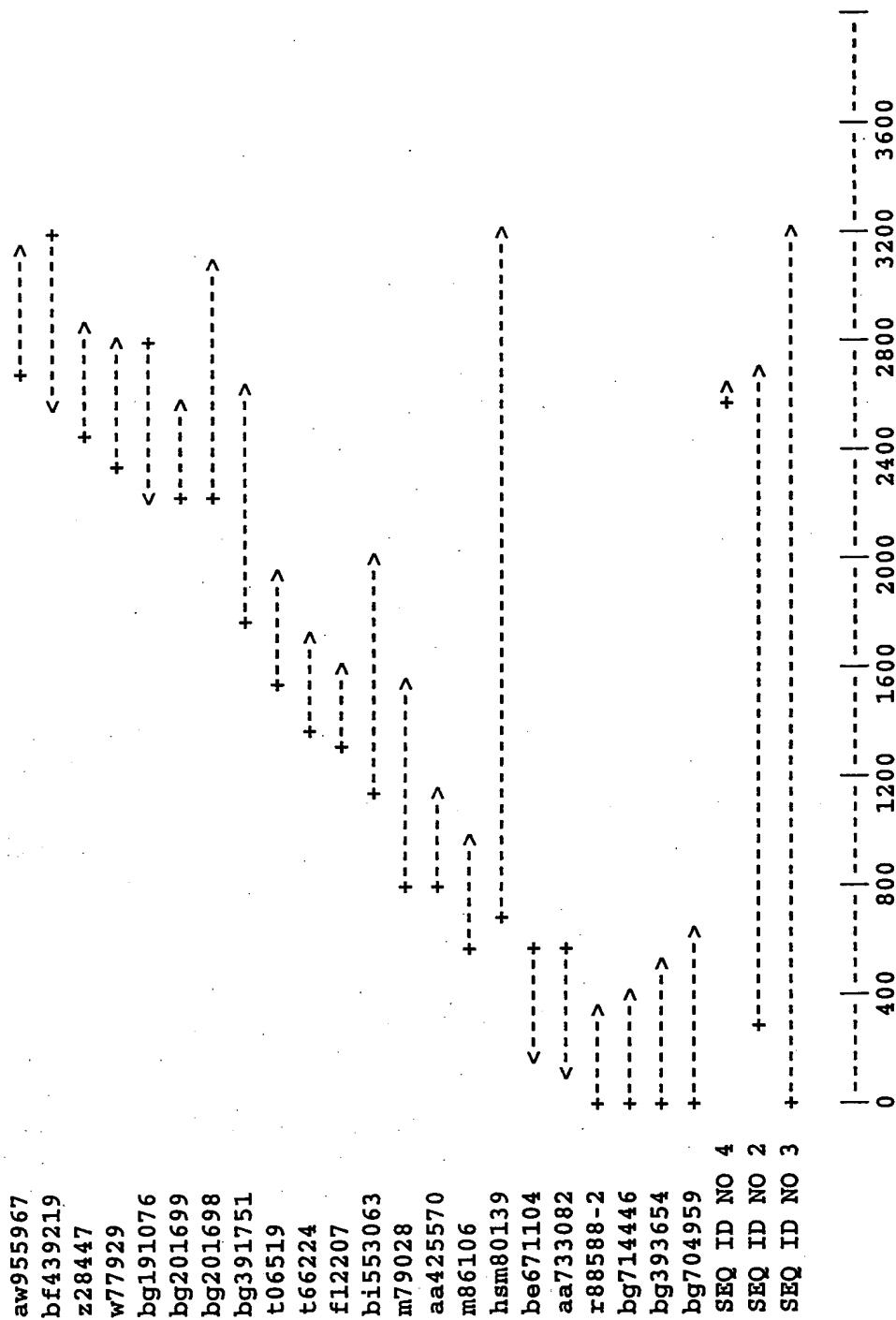
**Fig. 8: SEQ ID NO. 4**

**Length: 69 bp**

2471 ACAGCCAATCATGCTACCTAACCAGGCAGGTCAAGGGTCACTCCCAGCCA  
CTGGAATGCCTGTTTACTG 2539

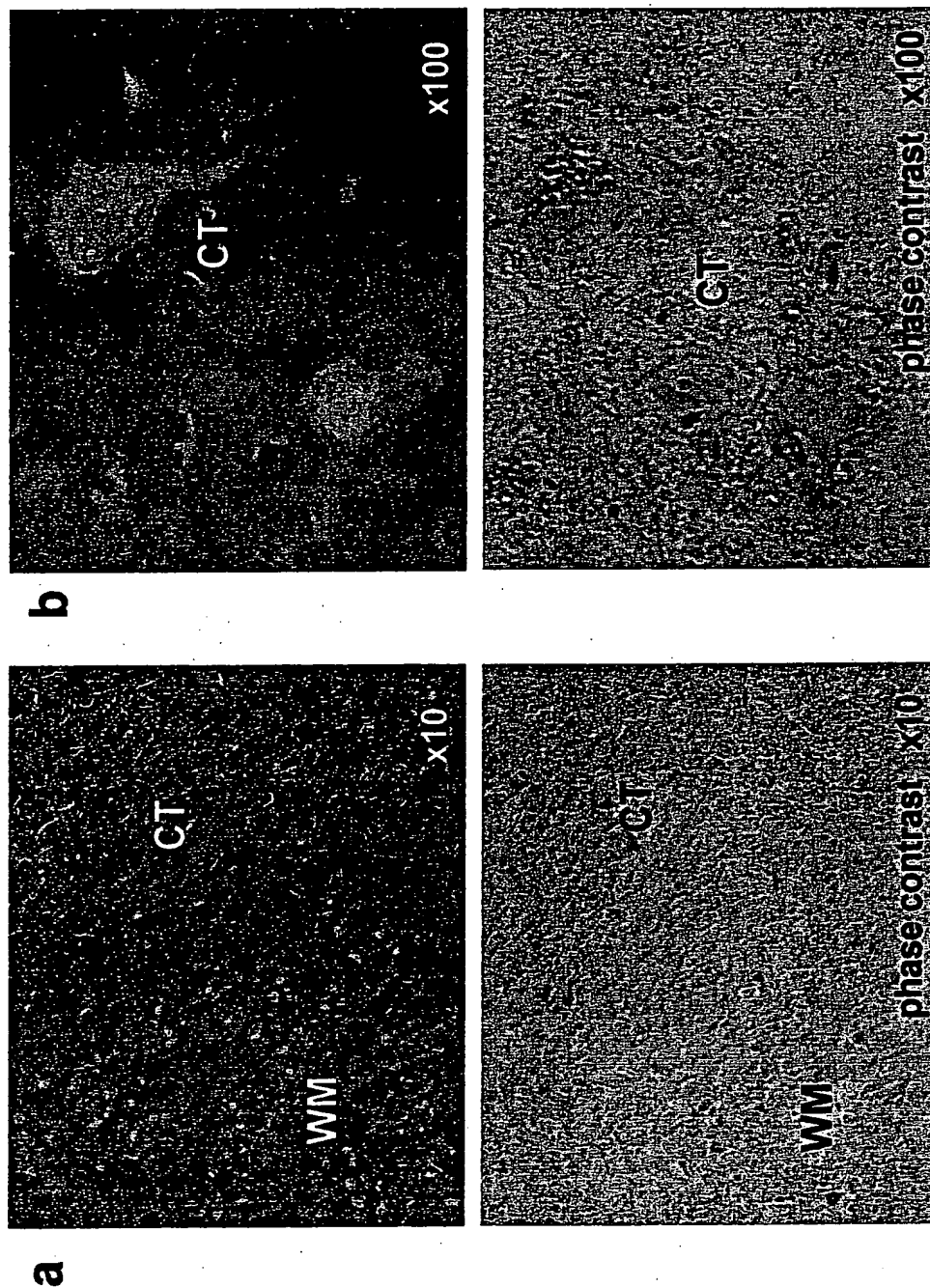
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**Fig. 9: Schematic alignment of SEQ ID NO. 3, SEQ ID NO. 2 and SEQ ID NO. 4 with Genome Database EST-cluster**



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**Fig. 10: Images of the human cerebral cortex  
labeled with anti-hTARPP antiserum and  
with DAPI**



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**Table 1:**

sample	$\Delta$ (fold) (frontal / temporal cortex)
<hr/>	
patient P012	2.21
patient P016	1.90
patient P010	4.11
patient P011	2.30
patient P014	1.73
patient P017	1.34
patient P019	2.62
control C011	1.24
control C012	1.15
control C014	0.47
control C005	1.39
control C008	1.38

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**Table 2:**

sample	$\Delta$ (fold) (frontal cortex / hippocampus)
<hr/>	
patient P012	1.50
patient P016	3.10
patient P010	5.51
patient P011	2.36
patient P014	1.21
patient P019	1.43
control C005	1.38
control C008	1.10
control C004	1.76